

## SEQUENCE LISTING

## 5 (1) GENERAL INFORMATION:

- (i) APPLICANT: Brodeur, Bernard R  
Martin, Denis  
Hamel, Josee  
10 Rioux, Clement
- (ii) TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN  
OF NEISSERIA MENINGITIDIS
- 15 (iii) NUMBER OF SEQUENCES: 26
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Goudreau Gage Dubuc & Martineau Walker  
(B) STREET: 800 Place Victoria, Suite 3400, Tour de la  
20 Eourse  
(C) CITY: Montreal  
(D) STATE: Quebec  
(E) COUNTRY: Canada  
(F) ZIP: H4Z 1E9
- 25 (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
30 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:  
35 (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/406,362  
(B) FILING DATE: 17-MAR-1995
- 40 (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US (PROVIS) 60/001,983  
(B) FILING DATE: 04-AUG-1995
- 45 (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Leclerc/Dubuc/Prince, Alain/Jean/Gaetan  
(C) REFERENCE/DOCKET NUMBER: BIOVAC-1 PCT
- (ix) TELECOMMUNICATION INFORMATION:  
50 (A) TELEPHONE: 514-397-7400  
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## 55 (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 830 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
60 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Neisseria meningitidis*  
 (B) STRAIN: 608B

10 (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 143..667

(ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 15 (B) LOCATION: 143..199

(ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 20 (B) LOCATION: 200..667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

25 TCGGCAAGGC AGCCGGATAC CGCTACGTAT CTTGAAGTAT TGAAAATATT ACGATGCAAA 60  
 AAAGAAAATT TAAGTATAAT ACAGCAGGAT TCTTTAACGG ATTCTTAACA ATTTTCTAA 120  
 CTGACCATAA AGGAACCAAA AT ATG AAA AAA GCA CTT GCC ACA CTG ATT GCC 172  
 Met Lys Lys Ala Leu Ala Thr Leu Ile Ala  
 30 -19 -15 -10

CTC GCT CTC CCG GCC GCC GCA CTG GCG GAA GGC GCA TCC GGC TTT TAC 220  
 Leu Ala Leu Pro Ala Ala Leu Ala Gly Gly Ala Ser Gly Phe Tyr  
 -5 1 5

35 GTC CAA GCC GAT GCC GCA CAC GCA AAA GCC TCA AGC TCT TTA GGT TCT 268  
 Val Gln Ala Asp Ala Ala His Ala Lys Ala Ser Ser Leu Gly Ser  
 10 15 20

40 GCC AAA GGC TTC AGC CCG CGC ATC TCC GCA GGC TAC CGC ATC AAC GAC 316  
 Ala Lys Gly Phe Ser Pro Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp  
 25 30 35

45 CTC CGC TTC GCC GTC GAT TAC ACG CGC TAC AAA AAC TAT AAA GCC CCA 364  
 Leu Arg Phe Ala Val Asp Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro  
 40 45 50 55

TCC ACC GAT TTC AAA CTT TAC AGC ATC GGC GCG TCC GCC ATT TAC GAC 412  
 Ser Thr Asp Phe Lys Leu Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp  
 50 60 65 70

TTC GAC ACC CAA TCG CCC GTC AAA CCG TAT CTC GGC GCG CGC TTG AGC 460  
 Phe Asp Thr Gln Ser Pro Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser  
 75 80 85

55 CTC AAC CGC GCC TCC GTC GAC TTG GGC GGC AGC GAC AGC TTC AGC CAA 508  
 Leu Asn Arg Ala Ser Val Asp Leu Gly Gly Ser Asp Ser Phe Ser Gln  
 90 95 100

60 ACC TCC ATC GGC CTC GGC GTA TTG ACG GGC GTA AGC TAT GCC GTT ACC 556  
 Thr Ser Ile Gly Leu Gly Val Leu Thr Gly Val Ser Tyr Ala Val Thr  
 105 110 115

CCG AAT GTC GAT TTG GAT GCC GGC TAC CGC TAC AAC TAC ATC GGC AAA 604  
 Pro Asn Val Asp Leu Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys 135  
 120 125 130

5 GTC AAC ACT GTC AAA AAC GTC CGT TCC GGC GAA CTG TCC GTC GGC GTG 652  
 Val Asn Thr Val Lys Asn Val Arg Ser Gly Glu Leu Ser Val Gly Val 150  
 140 145

10 CGC GTC AAA TTC TGATATGCGC CTTATTCTGC AAACCGCCGA GCCTTCGGCG 704  
 Arg Val Lys Phe 155

GTTTTGTTTT CTGCCACCGC AACTACACAA GCCGGCGGTT TTGTACGATA ATCCCGAATG 764

15 CTGCGGCTTC TGCCGCCCTA TTTTGTGAGG AATCCGAAT GTCCAAAACC ATCATCCACA 830  
 824  
 ACA

20 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 174 amino acids.  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Lys Ala Leu Ala Thr Leu Ile Ala Leu Ala Leu Pro Ala Ala  
 -19 -15 -10 -5

35 Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala  
 1 5 10

His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro  
 15 20 25

40 Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp  
 30 35 40 45

Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro Ser Thr Asp Phe Lys Leu  
 50 55 60

45 Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser Pro  
 65 70 75

50 Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Val  
 80 85 90

Asp Leu Gly Gly Ser Asp Ser Phe Ser Gln Thr Ser Ile Gly Leu Gly  
 95 100 105

55 Val Leu Thr Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp  
 110 115 120 125

Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys Asn  
 130 135 140

60 Val Arg Ser Gly Glu Leu Ser Val Gly Val Arg Val Lys Phe  
 145 150 155

## (2) INFORMATION FOR SEQ ID NO:3:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 710 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear
- 10 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 15 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Neisseria meningitidis  
 (B) STRAIN: MCH88
- 20 (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 116..643
- 25 (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 116..172
- (ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 173..643
- 30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

35 GTATCTTGAG GCATTGAAAA TATTACAATG CAAAAAGAAA ATTTTCAGTAT AATACGGCAG 60  
 GATTCTTTAA CGGATTCTTA ACCATTTTTC TCCCTGACCA TAAAGGAATC AAGAT ATG 118  
 Met  
 -19

40 AAA AAA GCA CTT GCC GCA CTG ATT GCC CTC GCC CTC CCG GCC GCC GCA 166  
 Lys Lys Ala Leu Ala Ala Leu Ile Ala Leu Ala Leu Pro Ala Ala Ala  
 -15 -10 -5

45 CTG GCG GAA GGC GCA TCC GGC TTT TAC GTC CAA GCC GAT GCC GCA CAC 214  
 Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala His  
 1 5 10

50 GCC AAA GCC TCA AGC TCT TTA GGT TCT GCC AAA GGC TTC AGC CCG CGC 262  
 Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro Arg  
 15 20 25 30

55 ATC TCC GCA GGC TAC CGC ATC AAC GAC CTC CGC TTC GCC GTC GAT TAC 310  
 Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp Tyr  
 35 40 45

ACG CGC TAC AAA AAC TAT AAA CAA GTC CCA TCC ACC GAT TTC AAA CTT 358  
 Thr Arg Tyr Lys Asn Tyr Lys Gln Val Pro Ser Thr Asp Phe Lys Leu  
 50 55 60

60 TAC AGC ATC GGC GCG TCC GCC ATT TAC GAC TTC GAC ACC CAA TCC CCC 406  
 Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser Pro  
 65 70 75

5 GTC AAA CCG TAT CTC GGC GCG CGC TTG AGC CTC AAC CGC GCC TCC GTC 454  
 Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Val  
 80 85 90  
 10 GAC TTT AAC GGC AGC GAC AGC TTC AGC CAA ACC TCC ACC GGC CTC GGC 502  
 Asp Phe Asn Gly Ser Asp Ser Phe Ser Gln Thr Ser Thr Gly Leu Gly  
 95 100 105 110  
 15 GCC GGC TAC CGC TAC AAC TAC ATC GGC AAA GTC AAC ACT GTC AAA AAT 598  
 Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys Asn  
 130 135 140  
 20 GTC CGT TCC GGC GAA CTG TCC GCC GGC GTA CGC GTC AAA TTC TGATATACGC 650  
 Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe  
 145 150 155  
 GTTATTCCGC AAACCGCCGA GCCTTTCGGC GGTTTTGTTC TCCGCCGCCG CAACTACACA 710

25

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 175 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Lys Lys Ala Leu Ala Ala Leu Ile Ala Leu Ala Leu Pro Ala Ala  
 -19 -15 -10 -5  
 40 Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala  
 1 5 10  
 His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro  
 15 20 25  
 45 Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp  
 30 35 40 45  
 50 Tyr Thr Arg Tyr Lys Asn Tyr Lys Gln Val Pro Ser Thr Asp Phe Lys  
 50 55 60  
 Leu Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser  
 65 70 75  
 55 Pro Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser  
 80 85 90  
 Val Asp Phe Asn Gly Ser Asp Ser Phe Ser Gln Thr Ser Thr Gly Leu  
 95 100 105  
 60 Gly Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu  
 110 115 120 125

Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys  
 130 135 140  
 5 Asn Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe  
 145 150 155

## (2) INFORMATION FOR SEQ ID NO:5:

- 10 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 850 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear
- 15 (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- 20 (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: *Neisseria meningitidis*  
 (B) STRAIN: 24063
- 25 (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 208..732
- 30 (ix) FEATURE:  
 (A) NAME/KEY: sig\_peptide  
 (B) LOCATION: 208..264
- 35 (ix) FEATURE:  
 (A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 265..732
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
- 40 CACCCATCCG CCGCGTGATG CCGCCACCAC CATTTAAAGG CAACGCGCGG GTTAACGGCT 60  
 TTGCCGTCCG CAAAGCAGCC GGATACCGCT ACGTATCTTG AAGTATTAAA AATATTACGA 120  
 45 TGCAAAAAGA AAATTTAAGT ATAATAAAGC AGAATTCTTT AACGGATTCT TAACAATTTT 180  
 TCTAACTGAC CATAAAGGAA CCAAAT ATG AAA AAA GCA CTT GCC ACA CTG 231  
 Met Lys Lys Ala Leu Ala Thr Leu  
 -19 -15
- 50 ATT GCC CTC GCT CTC CCG GCC GCC GCA CTG GCG GAA GGC GCA TCC GGC 279  
 Ile Ala Leu Ala Leu Pro Ala Ala Ala Leu Ala Glu Gly Ala Ser Gly  
 -10 -5 1 5
- 55 TTT TAC GTC CAA GCC GAT GCC GCA CAC GCA AAA GCC TCA AGC TCT TTA 327  
 Phe Tyr Val Gln Ala Asp Ala Ala His Ala Lys Ala Ser Ser Ser Leu  
 10 15 20
- 60 GGT TCT GCC AAA GGC TTC AGC CCG CGC ATC TCC GCA GGC TAC CGC ATC 375  
 Gly Ser Ala Lys Gly Phe Ser Pro Arg Ile Ser Ala Gly Tyr Arg Ile  
 25 30 35

AAC GAC CTC CGC TTC GCC GTC GAT TAC ACG CGC TAC AAA AAC TAT AAA 423  
 Asn Asp Leu Arg Phe Ala Val Asp Tyr Thr Arg Tyr Lys Asn Tyr Lys  
 40 45 50  
 5 GCC CCA TCC ACC GAT TTC AAA CTT TAC AGC ATC GGC GCG TCC GCC ATT 471  
 Ala Pro Ser Thr Asp Phe Lys Leu Tyr Ser Ile Gly Ala Ser Ala Ile  
 55 60 65  
 10 TAC GAC TTC GAC ACC CAA TCG CCC GTC AAA CCG TAT CTC GGC GCG CGC 519  
 Tyr Asp Phe Asp Thr Gln Ser Pro Val Lys Pro Tyr Leu Gly Ala Arg  
 70 75 80 85  
 15 TTG AGC CTC AAC CGC GCC TCC GTC GAC TTG GGC GGC AGC GAC AGC TTC 567  
 Leu Ser Leu Asn Arg Ala Ser Val Asp Leu Gly Gly Ser Asp Ser Phe  
 90 95 100  
 AGC CAA ACC TCC ACC GGC CTC GGC GTA TTG GCG GGC GTA AGC TAT GCC 615  
 Ser Gln Thr Ser Thr Gly Leu Gly Val Leu Ala Gly Val Ser Tyr Ala  
 105 110 115  
 20 GTT ACC CCG AAT GTC GAT TTG GAT GCC GGC TAC CGC TAC AAC TAC ATC 663  
 Val Thr Pro Asn Val Asp Leu Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile  
 120 125 130  
 25 GGC AAA GTC AAC ACT GTC AAA AAC GTC CGT TCC GGC GAA CTG TCC GCC 711  
 Gly Lys Val Asn Thr Val Lys Asn Val Arg Ser Gly Glu Leu Ser Ala  
 135 140 145  
 30 GGT GTG CGC GTC AAA TTC TGATATGCGC CTTATTCTGC AAACCGCCGA 759  
 Gly Val Arg Val Lys Phe  
 150 155  
 GCCTTCGGCG GTTTTGTTTT CTGCCACCGC AACTACACAA GCCGGCGGTT TTGTACGATA 819  
 35 ATCCCGAATG CTGCGGCTTC TGCCGCCCTA T 850

## (2) INFORMATION FOR SEQ ID NO:6:

40 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 174 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 45 (ii) MOLECULE TYPE: protein  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
 50 Met Lys Lys Ala Leu Ala Thr Leu Ile Ala Leu Ala Leu Pro Ala Ala  
 -19 -15 -10 -5  
 Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala  
 1 5 10  
 55 His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro  
 15 20 25  
 Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp  
 30 35 40 45  
 60 Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro Ser Thr Asp Phe Lys Leu  
 50 55 60

Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser Pro  
                     65                    70                    75  
 5 Val Lys Pro Tyr Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Val  
                     80                    85                    90  
 Asp Leu Gly Gly Ser Asp Ser Phe Ser Gln Thr Ser Thr Gly Leu Gly  
                     95                    100                    105  
 10 Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp  
                     110                    115                    120                    125  
 Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val Asn Thr Val Lys Asn  
                     130                    135                    140  
 15 Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe  
                     145                    150                    155

20 (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
     (A) LENGTH: 810 base pairs  
 25     (B) TYPE: nucleic acid  
     (C) STRANDEDNESS: double  
     (D) TOPOLOGY: linear  
  
 (ii) MOLECULE TYPE: DNA (genomic)  
 30 (iii) HYPOTHETICAL: NO  
     (iv) ANTI-SENSE: NO  
  
 (vi) ORIGINAL SOURCE:  
 35     (A) ORGANISM: Neisseria gonorrhoeae  
     (B) STRAIN: b2  
  
 (ix) FEATURE:  
 40     (A) NAME/KEY: CDS  
     (B) LOCATION: 241..765  
  
 (ix) FEATURE:  
     (A) NAME/KEY: sig\_peptide  
 45     (B) LOCATION: 241..297  
  
 (ix) FEATURE:  
     (A) NAME/KEY: mat\_peptide  
     (B) LOCATION: 298..765

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCCC GCCTTT GCGGTTTTT CCAAACCGTT TGCAAGTTTC ACCCATCCGC CGCGTGATGC 60  
 55 CGCCGTTTAA GGGCAACGCG CGGGTTAACG GATTGCGCGT CGGCAAAGCA GCCGGATGCC 120  
 GCCGCGTATC TTGAGGCATT GAAATATTA CGATGCAAAA AGAAAATTTT AGTATAATAC 180  
 GGCAGGATTC TTTAACGGAT TATTAACAAT TTTTCTCCCT GACCATAAAG GAACCAAAAT 240  
 60 ATG AAA AAA GCA CTT GCC GCA CTG ATT GCC CTC GCA CTC CCG GCC GCC 288  
 Met Lys Lys Ala Leu Ala Ala Leu Ile Ala Leu Ala Leu Pro Ala Ala  
   -19                    -15                    -10                    -5



GCA CTG GCG GAA GGC GCA TCC GGC TTT TAC GTC CAA GCC GAT GCC GCA 336  
 Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala  
 1 5 10  
 5 CAC GCC AAA GCC TCA AGC TCT TTA GGT TCT GCC AAA GGC TTC AGC CCG 384  
 His Ala Lys Ala Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro  
 15 20 25  
 10 CGC ATC TCC GCA GGC TAC CGC ATC AAC GAC CTC CGC TTC GCC GTC GAT 432  
 Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp  
 30 35 40 45  
 15 TAC ACG CGC TAC AAA AAC TAT AAA GCC CCA TCC ACC GAT TTC AAA CTT 480  
 Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro Ser Thr Asp Phe Lys Leu  
 50 55 60  
 20 TAC AGC ATC GGC GCG TCC GTC ATT TAC GAC TTC GAC ACC CAA TCG CCC 528  
 Tyr Ser Ile Gly Ala Ser Val Ile Tyr Asp Phe Asp Thr Gln Ser Pro  
 65 70 75  
 25 GTC AAA CCG TAT TTC GGC GCG CGC TTG AGC CTC AAC CGC GCT TCC GCC 576  
 Val Lys Pro Tyr Phe Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Ala  
 80 85 90  
 CAC TTG GGC GGC AGC GAC AGC TTC AGC AAA ACC TCC GCC GGC CTC GGC 624  
 His Leu Gly Gly Ser Asp Ser Phe Ser Lys Thr Ser Ala Gly Leu Gly  
 95 100 105  
 30 GTA TTG GCG GGC GTA AGC TAT GCC GTT ACC CCG AAT GTC GAT TTG GAT 672  
 Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp  
 110 115 120 125  
 35 GCC GGC TAC CGC TAC AAC TAC GTC GGC AAA GTC AAC ACT GTC AAA AAC 720  
 Ala Gly Tyr Arg Tyr Asn Tyr Val Gly Lys Val Asn Thr Val Lys Asn  
 130 135 140  
 GTC CGT TCC GGC GAA CTG TCC GCC GGC GTG CGC GTC AAA TTC TGATATACGC 772  
 Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe  
 145 150 155  
 GTTATTCGCG AAACCGCCGA GCCTTCGGCG GTTTTTCG 810

45 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

55 Met Lys Lys Ala Leu Ala Ala Leu Ile Ala Leu Ala Leu Pro Ala Ala  
 -19 -15 -10 -5

60 Ala Leu Ala Glu Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala  
 1 5 10

His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly Phe Ser Pro  
 15 20 25

Arg Ile Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp  
 30 35 40 45  
 5 Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro Ser Thr Asp Phe Lys Leu  
 50 55 60  
 Tyr Ser Ile Gly Ala Ser Val Ile Tyr Asp Phe Asp Thr Gln Ser Pro  
 65 70 75  
 10 Val Lys Pro Tyr Phe Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Ala  
 80 85 90  
 His Leu Gly Gly Ser Asp Ser Phe Ser Lys Thr Ser Ala Gly Leu Gly  
 95 100 105  
 15 Val Leu Ala Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp  
 110 115 120 125  
 20 Ala Gly Tyr Arg Tyr Asn Tyr Val Gly Lys Val Asn Thr Val Lys Asn  
 130 135 140  
 Val Arg Ser Gly Glu Leu Ser Ala Gly Val Arg Val Lys Phe  
 145 150 155  
 25

## (2) INFORMATION FOR SEQ ID NO:9:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 16 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 35 (ii) MOLECULE TYPE: protein  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Neisseria meningitidis  
 (B) STRAIN: 608B

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

45 Met Lys Lys Ala Leu Ala Thr Leu Ile Ala Leu Ala Leu Pro Ala Ala  
 1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:10:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 55 (ii) MOLECULE TYPE: protein  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: Neisseria meningitidis  
 (B) STRAIN: 608B  
 60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

5           Leu Ala Leu Pro Ala Ala Ala Leu Ala Glu Gly Ala Ser Gly Phe  
            1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

15

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Neisseria meningitidis  
(B) STRAIN: 608B

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

25           Gly Ala Ser Gly Phe Tyr Val Gln Ala Asp Ala Ala His Ala Lys  
            1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

35

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Neisseria meningitidis  
(B) STRAIN: 608B

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

45           Ala Ala His Ala Lys Ala Ser Ser Ser Leu Gly Ser Ala Lys Gly  
            1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

55

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Neisseria meningitidis  
(B) STRAIN: 608B

60

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Ser Ala Lys Gly Phe Ser Pro Arg Ile Ser Ala Gly Tyr Arg  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Neisseria meningitidis  
(B) STRAIN: 608B

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser Ala Gly Tyr Arg Ile Asn Asp Leu Arg Phe Ala Val Asp Tyr  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Neisseria meningitidis  
(B) STRAIN: 608B

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Phe Ala Val Asp Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro Ser Thr  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Neisseria meningitidis  
(B) STRAIN: 608B

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Tyr Lys Ala Pro Ser Thr Asp Phe Lys Leu Tyr Ser Ile Gly Ala  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Neisseria meningitidis  
(B) STRAIN: 608B

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Tyr Ser Ile Gly Ala Ser Ala Ile Tyr Asp Phe Asp Thr Gln Ser  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Neisseria meningitidis  
(B) STRAIN: 608B

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Phe Asp Thr Gln Ser Pro Val Lys Pro Tyr Leu Gly Ala Arg Leu  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Neisseria meningitidis  
(B) STRAIN: 608B

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Leu Gly Ala Arg Leu Ser Leu Asn Arg Ala Ser Val Asp Leu Gly  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:20:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- 10 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Neisseria meningitidis  
(B) STRAIN: 608B
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:  
Ser Val Asp Leu Gly Gly Ser Asp Ser Phe Ser Gln Thr Ser Ile  
1 5 10 15

## 20 (2) INFORMATION FOR SEQ ID NO:21:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- 30 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Neisseria meningitidis  
(B) STRAIN: 608B
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:  
Ser Gln Thr Ser Ile Gly Leu Gly Val Leu Thr Gly Val Ser Tyr  
1 5 10 15

## 40 (2) INFORMATION FOR SEQ ID NO:22:

- 45 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- 50 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Neisseria meningitidis  
(B) STRAIN: 608B
- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:  
Thr Gly Val Ser Tyr Ala Val Thr Pro Asn Val Asp Leu Asp Ala  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:23:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

10

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*  
(B) STRAIN: 608B

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Val Asp Leu Asp Ala Gly Tyr Arg Tyr Asn Tyr Ile Gly Lys Val  
1 5 10 15

20

## (2) INFORMATION FOR SEQ ID NO:24:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

30

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*  
(B) STRAIN: 608B

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Tyr Ile Gly Lys Val Asn Thr Val Lys Asn Val Arg Ser Gly Glu  
1 5 10 15

40

## (2) INFORMATION FOR SEQ ID NO:25:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 14 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

50

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Neisseria meningitidis*  
(B) STRAIN: 608B

55

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Val Arg Ser Gly Glu Leu Ser Val Gly Val Arg Val Lys Phe  
1 5 10

60

## (2) INFORMATION FOR SEQ ID NO:26:

## (i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 25 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

10

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Neisseria meningitidis  
(B) STRAIN: 608B

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

20

Phe Ala Val Asp Tyr Thr Arg Tyr Lys Asn Tyr Lys Ala Pro Ser Thr  
1 5 10 15  
Asp Phe Lys Leu Tyr Ser Ile Gly Ala  
20 25